

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 19:48:26 ; Search time 251 seconds

(without alignments)
13063.385 Million cell updates/sec

Title: US-09-919-197-3

Perfect score: 1456

Sequence: 1 tgagccagccgcaaccagg.....tatgaacactaaataaaaaa 1456

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

number of hits satisfying chosen parameters: 2331924

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_101002.*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 45 | 3.1 | 65 | ABN52223 | Mouse spliced tran |
| 2 | 31.4 | 2.2 | 49 | AAT89492 | CFTR binding site |
| 3 | 27.8 | 1.9 | 60 | ABN49410 | Human spliced tran |
| 4 | 27.6 | 1.9 | 47 | AA266146 | Human map-related |
| 5 | 26.2 | 1.8 | 47 | AA265699 | Human map-related |
| 6 | 26 | 1.8 | 73 | AA273834 | Human HER2 partial |
| 7 | 25.8 | 1.8 | 60 | ABN40794 | Human spliced tran |
| 8 | 25.4 | 1.7 | 47 | AAH38784 | Human SNP flanking |
| 9 | 25.4 | 1.7 | 60 | ABN39098 | Human spliced tran |

| | | | | | | |
|------|------|-----|----|----|----------|--------------------|
| c 10 | 25.4 | 1.7 | 72 | 19 | AAT97276 | Nucleotide EP-13 S |
| c 11 | 25.2 | 1.7 | 65 | 24 | ABN28389 | Rat spliced trans |
| c 12 | 25 | 1.7 | 51 | 22 | AAL30738 | Human SNP oligonuc |
| c 13 | 24.8 | 1.7 | 47 | 21 | AA267790 | Human map-related |
| c 14 | 24.6 | 1.7 | 60 | 24 | ABN47816 | Human spliced tran |
| c 15 | 24.4 | 1.7 | 51 | 22 | AAL30269 | Human SNP oligonuc |
| c 16 | 24 | 1.6 | 60 | 24 | ABN39375 | Human spliced tran |
| c 17 | 24 | 1.6 | 65 | 24 | ABN28030 | Rat spliced trans |
| c 18 | 23.8 | 1.6 | 64 | 21 | AAAL1650 | Humanised anti-Fas |
| c 19 | 23.8 | 1.6 | 64 | 24 | ABL46029 | Humanised anti-Fas |
| c 20 | 23.8 | 1.6 | 75 | 9 | AAH80654 | 75-mer probe used |
| c 21 | 23.6 | 1.6 | 47 | 21 | AA266638 | Human map-related |
| c 22 | 23.6 | 1.6 | 50 | 22 | AAL31451 | Human SNP oligonuc |
| c 23 | 23.6 | 1.6 | 60 | 18 | AAT61582 | VH and scFv antibo |
| c 24 | 23.6 | 1.6 | 60 | 24 | ABN32752 | Human spliced tran |
| c 25 | 23.6 | 1.6 | 60 | 24 | ABN32853 | Human spliced tran |
| c 26 | 23.6 | 1.6 | 60 | 24 | ABN59247 | Human spliced tran |
| c 27 | 23.6 | 1.6 | 71 | 18 | AAT92616 | SELEX-derived nucl |
| c 28 | 23.6 | 1.6 | 71 | 18 | AAT78604 | Class I SELEX gene |
| c 29 | 23.6 | 1.6 | 71 | 18 | AAT59094 | Human chorionic go |
| c 30 | 23 | 1.6 | 23 | 24 | ABL45019 | Human chromosome 1 |
| c 31 | 23 | 1.6 | 51 | 22 | AAL29070 | Human SNP oligonuc |
| c 32 | 23 | 1.6 | 60 | 21 | AAC23790 | Human secreted pro |
| c 33 | 22.6 | 1.6 | 50 | 22 | AAH89731 | Human coding sequ |
| c 34 | 22.6 | 1.6 | 60 | 24 | ABN32873 | Human spliced tran |
| c 35 | 22.6 | 1.6 | 60 | 24 | ABN34691 | Human spliced tran |
| c 36 | 22.6 | 1.6 | 64 | 22 | ABF80440 | 5-enolpyruvylshiki |
| c 37 | 22.6 | 1.6 | 69 | 15 | AA044415 | Special At-rich (A |
| c 38 | 22.4 | 1.5 | 50 | 22 | AAH89839 | Human coding sequ |
| c 39 | 22.4 | 1.5 | 60 | 24 | ABN44442 | Human spliced tran |
| c 40 | 22.4 | 1.5 | 68 | 22 | AAL02305 | Human reproductive |
| c 41 | 22.2 | 1.5 | 43 | 21 | AAH75934 | PCR primer used to |
| c 42 | 22.2 | 1.5 | 48 | 22 | AAH22252 | Anti-A33 antigen a |
| c 43 | 22.2 | 1.5 | 48 | 22 | AAH20117 | Rabbit anti A33 an |
| c 44 | 22.2 | 1.5 | 55 | 19 | AAV70103 | Humanised HFE7A he |
| c 45 | 22.2 | 1.5 | 55 | 20 | AAH01319 | Allelic ladder, HU |

ALIGNMENTS

RESULT 1

ABN52223

ID ABN52223 standard; DNA; 65 BP.

XX AC ABN52223;

XX AC ABN52223;

DT 15-JUL-2002 (first entry)

XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:24971.

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:24971.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KW splice variant; transcriptome; oligonucleotide library; ss.

XX Mus musculus.

OS Mus musculus.

PN WO200210449-A2.

XX 07-FEB-2002.

PD 20-JUL-2001; 2001WO-IB01903.

XX 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

DR New oligonucleotide libraries comprising oligonucleotides which

XX selectively hybridize to mRNAs transcribed from a transcription unit of

PT

Fri NOV 1 18:25:06 2002

PT a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes
PS Example 1; SEQ ID 24971; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialized mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological
XX condition; to detect developmental specific genes; and to detect RNA
XX transcripts and splice variants of a transcriptome of a patient suffering
XX from a particular disorder. AAN27253 to AAN59589 represent
XX oligonucleotide sequences from rats, humans and mice, which are used in
XX the exemplification of the present invention.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 65 BP; 15 A; 18 C; 14 G; 18 T; 0 other;

Query Match 3.1%; Score 45; DB 24; Length 65;
Best Local Similarity .83.6%; Pred. No. 0.004;
Matches 51; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1017 GACCTCTCTTCGCGCTATCATTTGGAGATGTTGACATCGCTGCTTCTTTGGGACATG 1076
DB 5 GATCTCTCTTCGCGCTATCATTTGGAGATGTTGACATCGCTGCTTCTTTGGGACATG 64

QY 1077 C 1077

DB 65 C 65

RESULT 2
AAT89492/c
AAT89492 standard; DNA; 49 BP.

AAT89492;

XX 14-APR-1998 (first entry)

XX CFTR binding site fragment 3.

XX Cystic fibrosis transmembrane conductance regulator; CFTR; gene therapy;
XX protein binding site; nuclear extract; gene promoter; cystic fibrosis;
XX spatial expression regulator; CF; ss.

XX Homo sapiens.

XX WO9735005-A2.

XX 25-SEP-1997

XX 20-MAR-1997; 97WO-GB00787.

XX 20-MAR-1996; 96GB-0005808.

XX (ISIS-) ISIS INNOVATION LTD.

XX Harris A;

XX

WPI; 1997-480211/44.

XX New oligo:nucleotide(s) for gene therapy of cystic fibrosis - are
XX able to increase the activity of the CF trans-membrane conductance
XX regulator gene promoter

XX Claim 3; Page 16; 20pp; English.

XX This sequence represents a minimum sequence required for binding of
XX proteins found in the nuclear extracts of cystic fibrosis transmembrane
XX conductance regulator (CFTR)-expressing cells. This sequence is an
XX oligonucleotide of the invention. This sequence, and sequences containing
XX it increase the activity of the CFTR gene promoter, so regulate spatial
XX expression of this gene (unlike viral or other promoters used in gene
XX therapy). Constructs containing this sequence are used in gene therapy of
XX cystic fibrosis (CF).

XX Sequence 49 BP; 15 A; 10 C; 5 G; 19 T; 0 other;

Query Match 2.2%; Score 31.4; DB 18; Length 49;

Best Local Similarity 77.6%; Pred. No. 32;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 557 AAGTCAGCTTGCCCAAGGTCACCCAGCTAATAAGTCACAGTCTGGGATT 605
DB 49 AAGTAAATTGCTTAGATCACATTCTTTAATAAGTCACAGTCTGGGATT 1

RESULT 3

ABN49410/c

ID ABN49410 standard; DNA; 60 BP.

XX AC ABN49410;

XX DT 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide. SEQ ID NO:22158.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB01903.

XX 28-JUL-2000; 2000US-221607P.

XX 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes

XX Example 1; SEQ ID 22158; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a

primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.

N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention.

```
Query Match      : 1.9%; Score 27.6; DB 21; Length 47;
Best Local Similarity 78.6%; Pred. No. 4e+02;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

Qy 554 ATTAAGTGACTTGGCCCAAGGTCACCCAGCTAATAAGTGACAG 595
||||| ||||| ||||| ||| ||||| |
Db 47 ATTAAGTCACTTGGCCCAAGGTATCCCCATTATAAGTAGCTG 6

ID AAZ65699 standard; DNA; 47 BP.

| | |
|----|------------------------------------|
| DT | 11-SEP-2001 (first entry) |
| XX | |
| DE | Human map-related biallelic marker |

Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.

Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW diagnosis; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

| | | |
|----|---------------|--------------------------------------|
| FT | Key variation | Location/Qualifiers replace(24,C) |
| FH | | |

```
FT /'tag= a
FT /standard_name= "single nucleotide polymorphism"
```

PN WO9954500-A2.

28-OCT-1999.

21-APR-1999. 99WQ-TB00822

PR 21-APR-1998: 98US-0082614.

XX
XX

PI Cohen D, Blumenfeld M, Chumakov I:

WPT: 2000-013267/01

PT Novel biallelic markers used to construct a high density disequilibrium map of the human genome -

PS Claim 1: page 240: 2745pp: English

AAZ65654 to AAZ69578 represent human biallelic markers from the present CC
CC invention, which contain a polymorphic base at position 24 of their CC
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification CC
CC primers for the biallelic markers. The biallelic markers of the CC
CC invention have a variety of uses: they can be used for high density CC
CC mapping of the human genome, and in complex association studies and CC

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CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 60 BP; 16 A; 15 C; 11 G; 18 T; 0 other;

Query Match 1.8%; Score 25.8; DB 24; Length 60;

Best Local Similarity 73.3%; Pred. No. 1.5e+03;

Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 562 ACTTCCCAAGTCAACCCAGCTAATAAGTGACAGTCTGGGATTC 606

Db 60 ACTGGCTCTAGATCATGTAGCAATTAAGTGACAGAGCTGTGAATC 16

LT 8

AAH38784

ID AAH38784 standard; DNA; 47 BP.

XX AC AAH38784;

DT 14-AUG-2001 (first entry)

DE Human SNP flanking oligonucleotide SEQ ID 1580.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; ds.

OS Homo sapiens.

XX WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US28436.

PR 15-OCT-1999; 99US-0160096.

XX (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample

XX Claim 1; Page 58; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.

CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
CC DNA flanking the site of a single nucleotide polymorphism.

XX Sequence 47 BP; 12 A; 15 C; 11 G; 9 T; 0 other;

Query Match 1.7%; Score 25.4; DB 22;

Best Local Similarity 74.4%; Pred. No. 1.8e+03;

Matches 32; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 550 AGAGATTAAAGTACCTTGCCCAAGGTCACCCAGCTAATAAGTGA 592

Db 4 AGAGGTCCAGCCACTTGCCCAAGGTCACACAGCTCTATTGCA 46

RESULT 9

ID ABN39098/c

XX ABN39098 standard; DNA; 60 BP.

AC ABN39098;

XX 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:11846.

KW Human; mouse; rat; splice transcript; detection; RNA transcript;

XX splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

XX WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB01903.

PR 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes

XX Example 1; SEQ ID 11846; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the

QY 1081 TGCTCAGGTGCACCTGTTCCAGCCCGCCAGAGATCAGGTGGCGCAGAGGCTG 1131

QY 707 AGGAGGAGGTAGTAGTGGGACCTCAAAGCCGAGCAAGAGGCGAG 752

RESULT 12

AAAL30738/c
ID AAL30738 standard; DNA; 51 BP.

XX
XX
AC AAL30738;

XX
DT 24-JAN-2002 (first entry)

XX
DE Human SNP oligonucleotide #3946.

XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

XX
Homo sapiens.

PN
WO200147944-A2.

XX
PD 05-JUL-2001.

XX
PF 28-DEC-2000; 2000WO-US35498.

XX
PR 28-DEC-1999; 99US-0173419.

XX
PR 27-DEC-2000; 2000US-0173419.

XX
PA (CURA-) CURAGEN CORP.

XX
PI Shimkets RA, Leach M;

XX
DR WPT; 2001-465210/50.

XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections

XX
PS Claim 1; Page 2520; 4143pp; English.

XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

XX
SQ Sequence 51 BP; 13 A; 5 C; 1 G; 32 T; 0 other;

Query Match

Best Local Similarity 1.7%; Score 25; DB 22; Length 51;

Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1408 APTAAGTATTGATTTTGTATTAAGGTATGAACACTAAAAA 1456

DB 49 AGTAAAGTGCTATTATTTGTAGTAAAAA 1

RESULT 13

AAZ67790

ID AAZ67790 standard; DNA; 47 BP.

XX
AC AAZ67790;

XX
DT 10-SEP-2001 (first entry)

XX
DE Human map-related biallelic marker SEQ ID NO:2137.

XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.

OS
Homo sapiens.

XX
FH Key Location/Qualifiers

FT variation replace(24,G)

FT /*tag= a

FT /standard_name= "single nucleotide polymorphism"

XX
PN WO9954500-A2.

XX
PD 28-OCT-1999.

XX
PF 21-APR-1999; 99WO-IB00822.

XX
PR 21-APR-1998; 98US-0082614.

XX
PR 23-NOV-1998; 98US-0109732.

XX
PA (GEST) GENSET.

XX
PI Cohen D, Blumenfeld M, Chumakov I;

XX
DR WPT; 2000-013267/01.

XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome

XX
PS Claim 1; Page 686; 2745pp; English.

XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.

XX
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.

XX
SQ Sequence 47 BP; 16 A; 10 C; 11 G; 10 T; 0 other;

Query Match

Best Local Similarity 1.7%; Score 24.8; DB 21; Length 47;

Matches 32; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 550 AGAGATTAAAGTGACTTGCACCAAGGTACCCAGCTCAATTAAGTGAC 593

DB 3 AGAAACAAGGAGACTTGCACCAAGGTCTGTCATCAATTAAGTGCC 46

RESULT 14

ABN47816

ID ABN47816 standard; DNA; 60 BP.

XX
AC ABN47816;

XX DT 15-JUL-2002 (first entry)
 XX DE Human spliced transcript-detection oligonucleotide SEQ ID NO:20564.
 XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 XX KW splice variant; transcriptome; oligonucleotide library; ss.
 XX OS Homo sapiens
 XX PN WO200210449-A2.
 XX PD 07-FEB-2002.
 XX PF 20-JUL-2001; 2001WO-IB01903.
 XX PR 28-JUL-2000; 2000US-221607P.
 XX PR 02-MAY-2001; 2001US-287724P.
 XX (COMP-) COMPUGEN INC.
 XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX WPI; 2002-257383/30..
 XX New oligonucleotide libraries comprising oligonucleotides which
 XX selectively hybridize to mRNAs transcribed from a transcription unit of
 XX a genome, useful for detecting tissue-, pathology-, and
 XX developmental-specific genes
 XX Example 1; SEQ ID 20564; 47pp; English.
 XX The present invention describes oligonucleotide libraries for detecting
 XX messenger RNAs that populate a (sub-)transcriptome, where the
 XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 XX transcription units that populate a genome. The library comprises
 XX several oligonucleotides, each capable of hybridizing selectively to a
 XX set of messenger RNAs transcribed from a given transcription unit of
 XX the genome, which encodes one or more messenger RNA splice variants.
 XX The oligonucleotide libraries are useful for detecting mRNAs from a
 XX biological sample, in expression profiling studies, in qualitatively or
 XX quantitatively characterising the corresponding transcriptome, and in
 XX detecting RNA transcripts and splice variants of human or animal
 XX transcriptomes. The libraries may also be used as specialised mini
 XX libraries to detect transcripts of a sub-transcriptome under a
 XX particular biological or pathological state, and so allowing the
 XX detection of tissue- and pathology-specific genes such as those genes
 XX only expressed in specific tissue under a specific pathological
 XX condition; to detect developmental specific genes; and to detect RNA
 XX transcripts and splice variants of a transcriptome of a patient suffering
 XX from a particular disorder. ABN27253 to ABN59589 represent
 XX oligonucleotide sequences from rats, humans and mice, which are used in
 XX the exemplification of the present invention.
 XX N.B. The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 60 BP; 20 A; 13 C; 15 G; 12 T; 0 other;
 XX Query Match 1.7%; Score 24.6; DB 24; Length 60;
 XX Best Local Similarity 65.5%; Pred. No. 3.5e+03;
 XX Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 547 CCAGAGATTAGTGGCCAGCTGACCCAGCTAATAGTGACAGTGCTGG 601
 DB 1 CCTAGAGTTAGTTACTGCTCAAGACACAGTAGCTAGTAGGACGAGCCAGG 55
 RESULT 15
 AAL30269/C
 ID AAL30269 standard; DNA; 51 BP.
 XX AAL30269;
 XX

XX DT 24-JAN-2002 (first entry)
 XX DE Human SNP oligonucleotide #3477.
 XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinasin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX OS Homo sapiens.
 XX PN WO200147944-A2.
 XX PD 05-JUL-2001.
 XX PF 28-DEC-2000; 2000WO-US35498.
 XX PR 28-DEC-1999; 99US-0173419.
 XX PR 27-DEC-2000; 2000US-0173419.
 XX (CURA-) CURAGEN CORP.
 XX Shimkets RA, Leach M;
 XX WPI; 2001-465210/50.
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 XX oncogenes and histones, useful for diagnosing and treating, e.g.
 XX cancer, autoimmune diseases and infections
 XX Claim 1; Page 2383; 4143pp; English.
 XX The present invention relates to oligonucleotides encoding polymorphic
 XX variants of proteins related to amylases, amyloid proteins, angiotensin,
 XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 XX histones, kinases, colony stimulating factors, complement related
 XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 XX G-protein coupled receptors and thioesterases. The present sequence is
 XX one such oligonucleotide. The oligonucleotides and the peptides encoded
 XX by them may be used in the prevention, diagnosis and treatment of
 XX diseases associated with inappropriate expression of the proteins listed
 XX above. Disorders that may be prevented, diagnosed and/or treated include
 XX multifactorial diseases with a genetic component, such as autoimmune
 XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
 XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
 XX leukaemia), diseases of the nervous system and an infection of pathogenic
 XX organisms.
 XX Sequence 51 BP; 12 A; 1 C; 2 G; 36 T; 0 other;
 XX Query Match 1.7%; Score 24.4; DB 22; Length 51;
 XX Best Local Similarity 68.0%; Pred. No. 3.6e+03;
 XX Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 QY 1407 AATTAAGTATTGTTTGTAAATAAAGGTATGAACACATAAAAAA 1456
 DB 51 AATAAAATCTTATCTTTAGTAAAAAATAAAAAAATAAAAAA 2
 Search completed: October 31, 2002, 21:55:33
 Job time : 253 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 19:54:31 ; Search time 2921 Seconds
(without alignments)
14506.568 Million cell updates/sec

Title: US-09-919-197-3
Perfect score: 1456
Sequence: 1 tgaacaccagccaccagg.....tatgaacacataaaaaaa 1456

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues.
1 number of hits satisfying chosen parameters: 941340

Minimum DB seq length: 0
Maximum DB seq length: 75
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.fod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|-----------|--------------------|
| C 1 | 31.4 | 2.2 | 49 | 6 | A65431 | A65431 Sequence 23 |
| C 2 | 29.4 | 2.0 | 71 | 4 | AR055530 | AR055530 Didelphis |
| C 3 | 25.4 | 1.7 | 47 | 6 | AX116457 | AX116457 Sequence |
| C 4 | 25.4 | 1.7 | 72 | 6 | E14197 | E14197 PCR primer |
| C 5 | 24.6 | 1.7 | 64 | 9 | HS001823 | AJ001823 Homo sapi |
| C 6 | 23.8 | 1.6 | 64 | 6 | E40916 | E40916 Humanized a |
| C 7 | 23.8 | 1.6 | 75 | 6 | A05173 | A05173 Oligonucleo |
| C 8 | 23.6 | 1.6 | 60 | 6 | AR117953 | AR117953 Sequence |
| C 9 | 23.6 | 1.6 | 71 | 6 | AR020462 | AR020462 Sequence |
| C 10 | 23.6 | 1.6 | 71 | 6 | AR054774 | AR054774 Sequence |
| C 11 | 23.6 | 1.6 | 71 | 6 | AR066039 | AR066039 Sequence |
| C 12 | 23.4 | 1.6 | 75 | 6 | A15067 | A15067 Nucleotide |
| C 13 | 23 | 1.6 | 74 | 6 | A08223 | A08223 synthetic o |
| C 14 | 23 | 1.6 | 74 | 6 | A08224 | A08224 synthetic o |
| C 15 | 22.8 | 1.6 | 74 | 8 | CBE345111 | AJ345111 Carpinus |
| C 16 | 22.6 | 1.6 | 50 | 6 | AX199582 | AX199582 Sequence |
| C 17 | 22.6 | 1.6 | 65 | 6 | AX482787 | AX482787 Sequence |
| C 18 | 22.4 | 1.5 | 50 | 6 | AX199690 | AX199690 Sequence |
| C 19 | 22.4 | 1.5 | 54 | 6 | AR139994 | AR139994 Sequence |
| C 20 | 22.4 | 1.5 | 65 | 6 | AX485185 | AX485185 Sequence |
| C 21 | 22.2 | 1.5 | 48 | 6 | AR184251 | AR184251 Sequence |
| C 22 | 22.2 | 1.5 | 48 | 6 | AR184372 | AR184372 Sequence |
| C 23 | 22.2 | 1.5 | 48 | 6 | AX127963 | AX127963 Sequence |
| C 24 | 22.2 | 1.5 | 55 | 6 | AX002002 | AX002002 Sequence |
| C 25 | 22.2 | 1.5 | 55 | 6 | E40050 | E40050 Drug contai |
| C 26 | 22.2 | 1.5 | 55 | 6 | E40858 | E40858 Humanized a |
| C 27 | 22.2 | 1.5 | 55 | 6 | E43404 | E43404 Humanized a |
| C 28 | 22.2 | 1.5 | 61 | 6 | AR051730 | AR051730 Sequence |
| C 29 | 22.2 | 1.5 | 61 | 6 | AR117040 | AR117040 Sequence |
| C 30 | 22.2 | 1.5 | 61 | 6 | AR200053 | AR200053 Sequence |
| C 31 | 22.2 | 1.5 | 61 | 6 | I20500 | I20500 Sequence 22 |
| C 32 | 22.2 | 1.5 | 61 | 6 | I49676 | I49676 Sequence 20 |
| C 33 | 22.2 | 1.5 | 63 | 6 | BD002020 | BD002020 Construct |
| C 34 | 22.2 | 1.5 | 63 | 6 | I08751 | I08751 Sequence 13 |
| C 35 | 22.2 | 1.5 | 65 | 6 | AR117041 | AR117041 Sequence |
| C 36 | 22.2 | 1.5 | 65 | 6 | AR200054 | AR200054 Sequence |
| C 37 | 22.2 | 1.5 | 65 | 6 | I20501 | I20501 Sequence 23 |
| C 38 | 22.2 | 1.5 | 65 | 6 | I49677 | I49677 Sequence 21 |
| C 39 | 22.2 | 1.5 | 69 | 6 | I16689 | I16689 Sequence 21 |
| C 40 | 22.2 | 1.5 | 69 | 6 | I89442 | I89442 Sequence 29 |
| C 41 | 22.2 | 1.5 | 70 | 6 | AX328443 | AX328443 Sequence |
| C 42 | 22 | 1.5 | 39 | 6 | AX137540 | AX137540 Sequence |
| C 43 | 22 | 1.5 | 51 | 6 | AX162353 | AX162353 Sequence |
| C 44 | 22 | 1.5 | 58 | 6 | E03095 | E03095 RNA encodin |
| C 45 | 22 | 1.5 | 59 | 9 | S76156 | S76156 delta-beta |

ALIGNMENTS

RESULT 1
A65431/c
LOCUS A65431
DEFINITION Sequence 23 from Patent WO9735005.
ACCESSION A65431
VERSION A65431.1 GI:4531190
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 49)
AUTHORS Harris.A.
TITLE CFTR GENE REGULATOR
JOURNAL Patent: WO 9735005-A 23 25-SEP-1997;
ISIS INNOVATION (GB)

Linear PAT 29-MAR-1999

COMMENT Other publication AU 2036897 19971010.
FEATURES Location/Qualifiers
Source 1..49
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 12 a 15 c 11 g 9 t
ORIGIN
Query Match 1.7%; Score 25.4; DB 6; Length 47;
Best Local Similarity 74.4%; Pred. No. 8.1e+04;
Matches 32; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 550 AGAGTAAAGTCACTGCGCCAGGTCACCCAGCTAATAAGTGA 592
Db 4 AGAGTCCAGCCACTGCGCCAGGTCACCCAGCTAATAAGTGA 46
RESULT 4
E14197/c
LOCUS PCR primer for gaining C7 region epitope of HCV.
DEFINITION E14197
ACCESSION E14197
VERSION E14197.1 GI:5708880
KEYWORDS JP 1997278794-A/40.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 72)
AUTHORS Yamaguchi, K., Kashiwaguma, T., Chiba, Y., Yagi, S. and Hasegawa, A.
TITLE CHIMERA ANTIGEN PEPTIDE
JOURNAL Patent: JP 1997278794-A 40 28-OCT-1997;
TONE CORP.
COMMENT OS None
OC Artificial sequences.
PN JP 1997278794-A/40
PD 28-OCT-1997
PF 10-FEB-1997 JP 1997027015
PI 09-FEB-1996 JP 96P 24045
PI YAMAGUCHI KENJIRO, KASHIWAGUMA TOMIKO, CHIBA YUKIE, PI YAGI SHINTARO.
PI HASEGAWA AKIRA
PC C07K14/18,C07H21/04,C07K19/00,C12N15/09,C12P21/02,G01N33/53,
PC G01N33/576//
PC C12N1/21,(C12P21/02,C12R1:19),(C12N1/21,C12R1:19); CC
strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: Yes; Location/Qualifiers
FH Key
FT source 1..72
/organism="Artificial sequences"
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Source 1..72
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 15 a 25 c 21 g 11 t
ORIGIN
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Best Local Similarity 68.6%; Pred. No. 8.7e+04;
Matches 35; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 1081 TGCTCAGGTGACCTGTTCAGCCAGGAGAGATCAGGTGGCAGAGCTG 1131
Db 70.TGCTCGGTGACCTATTCCAGCTAGGTAATACCTGGCGGAGCGGGTTG 20
RESULT 5
HS001823
LOCUS Homo sapiens exon 2E4 from Los Alamos contig C159.1, chromosome
DEFINITION HS001823
AUTHORS 16p12.2
TITLE Patent: WO 0129262-A 1580 26-APR-2001;
JOURNAL AJ001823
VERSION AJ001823.1 GI:2462356
KEYWORDS

COMMENT Other publication AU 2036897 19971010.
FEATURES Location/Qualifiers
Source 1..49
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 15 a 10 c 5 g 19 t
ORIGIN
Query Match 2.2%; Score 31.4; DB 6; Length 49;
Best Local Similarity 77.6%; Pred. No. 1.8e+03;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 557 AAGTCACTGCGCCAGGTCACCCAGCTAATAAGTCACAGTCTGGGATT 605
Db 49 AAGTAAATGCTAGATCATCACTGTTAATAAGTCACAGAGTAGGATT 1
RESULT 2
AF055530/c
S Didelphis virginiana isolate O51 retroposon CORE-SINE Mar-1
NITION AF055530.1 GI:4511910
ACCESSION AF055530
VERSION AF055530
KEYWORDS Didelphis virginiana.
SOURCE Didelphis virginiana
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
REFERENCE 1 (bases 1 to 71)
AUTHORS Gilbert, N. and Labuda, D.
TITLE Evolutionary inventions and continuity of CORE-SINES in mammals
JOURNAL J. Mol. Biol. 298 (3), 365-377 (2000)
MEDLINE 20237720
PubMed 10772856
FEATURES Location/Qualifiers
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/isolate="O51"
/db_xref="taxon:9267"
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/rpt_family="retroposon CORE-SINE Mar-1"
/rpt_type="dispersed"
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ORIGIN
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Best Local Similarity 79.7%; Pred. No. 6.9e+03;
Matches 47; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
QY 529 CCGATAAGAACTGAGCCAGCA-GATTAAAGTCACTGCGCCAGGTCACCCAGCTAAT 586
Db 63 CAGATGAGAACTGAGCCAGCAAGGTGAATGACTGCGCCAGGTCACACAGCTAGT 5
RESULT 3
AX116457
LOCUS Sequence 1580 from Patent WO0129262.
DEFINITION AX116457
ACCESSION AX116457
VERSION AX116457.1 GI:14033399
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 47)
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1580 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES Location/Qualifiers
Source 1..47

| | | | |
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| QY | 952 | GCGCCTGTACCCGCTGTCCTCTCACGGCGCTTCCACCCTCAAGTCCAT | 997 |
| Db | 63 | GTGCTGTGCCACTGCCCTCCACGTCGTGCCCTCCACACTCAGGCCTTT | 18 |
| RESULT 12 | | | |
| LOCUS | AL5067 | 105 bp | DNA linear PAT 07-FEB-1994 |
| DEFINITION | Nucleotide sequence 8 from patent number EP0206863. | | |
| ACCESSION | AL5067 | | |
| VERSION | AL5067.1 | GI:492830 | |
| KEYWORDS | unidentified. | | |
| SOURCE | unclassified. | | |
| ORGANISM | unclassified. | | |
| REFERENCE | 1 (bases 1 to 75) | | |
| AUTHORS | Roskam, W. and Ferrara, P. | | |
| TITLE | Non-amidated derivatives of somatocrine and process for the preparation by genetic engineering | | |
| JOURNAL | Patent: EP 0206863-A 8 30-DEC-1986; | | |
| FEATURES | SANOFI S.A. | | |
| source | Location/Qualifiers | | |
| BASE COUNT | 17 a | 21 c | 24 g |
| ORIGIN | 1..75 /organism="unidentified" | | |
| | /db_xref="taxon:32644" 13 t | | |
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| Best Local Similarity | 67.3%; | Pred. No. 3 le+05; | |
| Matches | 33; Conservative | 0; Mismatches | 16; Indels 0; Gaps 0; |
| QY | 255 | C GGCTGTGTGAGGCTTGCTGGGGCCCCCTCTCTCTGCTGTGGGTGGGCC | 303 |
| Db | 75 | CGGATCTACAGCGGTGCACGGCGCCACGCTCTGTGTAGATTGCGCC | 27 |
| RESULT 13 | | | |
| LOCUS | A08223 | 74 bp | DNA linear PAT 19-JUL-1993 |
| DEFINITION | synthetic oligonucleotide primer Va. | | |
| ACCESSION | A08223 | | |
| VERSION | A08223.1 | GI:413428 | |
| KEYWORDS | synthetic construct. | | |
| SOURCE | synthetic construct | | |
| ORGANISM | artificial sequences. | | |
| REFERENCE | 1 (bases 1 to 74) | | |
| AUTHORS | Seemann, G., Bosslet, K. and Sedlacek, H.H. | | |
| TITLE | Antigens composed of major histocompatibility complex class I antigens and specific carrier molecules, their production and use | | |
| JOURNAL | Patent: EP 0352761-A 5 31-JAN-1990; | | |
| FEATURES | BEHRINGWERKE Aktiengesellschaft | | |
| source | Location/Qualifiers | | |
| BASE COUNT | 15 a | 27 c | 25 g 7 t |
| ORIGIN | 1..74 /organism="synthetic construct" | | |
| | /db_xref="taxon:32630" | | |
| Query Match | 1.6%; | Score 23; | DB 6; Length 74; |
| Best Local Similarity | 68.1%; | Pred. No. 4e+05; | |
| Matches | 32; Conservative | 0; Mismatches | 15; Indels 0; Gaps 0; |
| QY | 229 | GGCAGCTGGCTCCCGAGGACACAGCGCGGCTGCTGCAGGGTTGCTGG | 275 |
| Db | 15 | GGCAGCTCCCGAGGCTGCACCGCGACGACCGCGCAGCGCGGCGAG | 61 |
| RESULT 14 | | | |
| LOCUS | A08224/c | 74 bp | DNA linear PAT 19-JUL-1993 |

DEFINITION synthetic oligonucleotide primer Vb.
ACCESSION A08224
VERSION A08224.1 GI:413429
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 74)
AUTHORS Seemann, G., Bosslet, K. and Sedlacek, H.H.
TITLE Antigens composed of major histocompatibility complex class I
antigens and specific carrier molecules, their production and use
JOURNAL Patent: EP 0352761-A 6 31-JAN-1990;
BEHRINGWERKE Aktiengesellschaft

FEATURES
Location/Qualifiers

1..74
source
/organism="synthetic construct"
/db_xref="taxon:32630" 15 t
BASE COUNT 7 a 25 c 27 g 15 t
ORIGIN

Query Match 1.6%; Score 23; DB 6; Length 74;
Best Local Similarity 68.1%; Pred. No. 4e+05;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 229 GGCAGCTGCTCCCGAGCAGCAGCGCGGCTGCTGCAGGGTTGCTGG 275
||||||| || | | | | | | | | | | | | | | | | | |
Db 60 GGCAGCTCCCGAGCTGTCACCCGAGCAGCGCAGCGCGGGCAGG 14

RESULT 15
CBE345111/c 74 bp DNA circular PLN 04-JAN-2002
LOCUS CBE345111
DEFINITION Carpinus betulus chloroplast microsatellite, ccmpl0 (3).
ACCESSION AJ345111
VERSION AJ345111.1 GI:18072971
KEYWORDS satellite.
ORGANISM Carpinus betulus
European hornbeam.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fagales; Betulaceae; Carpinus.

REFERENCE 1
AUTHORS Grivet, D. and Petit, R.J.
TITLE Chloroplast DNA phylogeography of the hornbeam in Europe: evidence
for a bottleneck at the outset of postglacial colonization
JOURNAL unpublished
REFERENCE 2 (bases 1 to 74)
AUTHORS Grivet, D.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2001) Grivet D., Recherches forestieres, Intra,
BP45, Gazinet Cedex, 33611, FRANCE
FEATURES Location/Qualifiers

1..74
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/organism="Carpinus betulus"
/db_xref="taxon:12990"
repeat_unit 17..32
/note="ccmpl0 (3)"
BASE COUNT 19 a 11 c 6 g 38 t
ORIGIN

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Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 1396 ATACAGAACTGAATTAGTATTGATTTTGTATTAAGGTATGAACTATAAAA 1453
||| || ||||| || | | | | | | | | | | | | | | | | | |
Db 72 ATAGAAATCGAATTGTTCTCTTACAAAAAGAAAAAATAAATA 15

Search completed: October 31, 2002, 22:44:37
Job time : 2924 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 21:49:51 ; Search time 59 Seconds
(without alignments)

7568.159 Million cell updates/sec

Title: US-09-919-197-3

Perfect score: 1456

Sequence: 1 tgaaccagccaccaggg.....tatgaacactaataaaaaa 1456

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

1 number of hits satisfying chosen parameters: 662272

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| C 1 | 25.4 | 1.7 | 72 | 4 | US-09-020-846-51 |
| C 2 | 23.6 | 1.6 | 60 | 3 | US-08-983-607-45 |
| C 3 | 23.6 | 1.6 | 71 | 1 | US-08-487-425-2 |
| C 4 | 23.6 | 1.6 | 71 | 2 | US-08-488-402A-5 |
| C 5 | 23.6 | 1.6 | 71 | 2 | US-08-484-552A-5 |
| C 6 | 23.6 | 1.6 | 71 | 2 | US-08-628-356A-4 |
| C 7 | 23.6 | 1.6 | 71 | 5 | PCT-US96-07439-2 |
| C 8 | 23.6 | 1.6 | 71 | 5 | PCT-US96-09472-5 |
| C 9 | 22.4 | 1.5 | 54 | 4 | US-09-257-581-1 |
| C 10 | 22.2 | 1.5 | 48 | 4 | US-09-425-638A-38 |
| C 11 | 22.2 | 1.5 | 48 | 4 | US-09-543-004-38 |
| C 12 | 22.2 | 1.5 | 61 | 1 | US-07-609-716-22 |
| C 13 | 22.2 | 1.5 | 61 | 1 | US-08-175-155-20 |
| C 14 | 22.2 | 1.5 | 61 | 1 | US-08-477-509B-55 |
| C 15 | 22.2 | 1.5 | 61 | 1 | US-08-707-237A-26 |
| C 16 | 22.2 | 1.5 | 61 | 3 | US-08-482-085B-55 |
| C 17 | 22.2 | 1.5 | 61 | 3 | US-08-475-411A-22 |
| C 18 | 22.2 | 1.5 | 61 | 4 | US-08-478-029A-22 |
| C 19 | 22.2 | 1.5 | 61 | 4 | US-09-444-791A-55 |
| C 20 | 22.2 | 1.5 | 65 | 1 | US-07-609-716-23 |
| C 21 | 22.2 | 1.5 | 65 | 1 | US-08-175-155-21 |
| C 22 | 22.2 | 1.5 | 65 | 1 | US-08-477-509B-56 |
| C 23 | 22.2 | 1.5 | 65 | 3 | US-08-482-085B-56 |
| C 24 | 22.2 | 1.5 | 65 | 3 | US-08-475-411A-23 |
| C 25 | 22.2 | 1.5 | 65 | 4 | US-08-478-029A-23 |
| C 26 | 22.2 | 1.5 | 65 | 4 | US-09-444-791A-56 |
| C 27 | 22.2 | 1.5 | 69 | 1 | US-07-991-867B-29 |

Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
Patent No. 5436330
Sequence 4, Appl
Sequence 17, Appl
Sequence 21, Appl
Sequence 928, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 26, Appl
Sequence 39, Appl
Sequence 172, Appl
Sequence 20, Appl
Sequence 13, Appl

69 1 US-08-107-755A-29
69 2 US-08-544-332-29
69 4 US-09-370-861A-29
58 6 5436330-3
61 1 US-08-055-390-4
75 4 US-09-042-353-173
75 4 US-08-758-417A-21
47 4 US-09-641-638-928
71 2 US-08-488-402A-28
71 2 US-08-484-552A-28
71 5 PCT-US96-09472-28
54 2 US-08-412-376-12
54 2 US-08-412-376-26
63 5 PCT-US94-06079-39
70 4 US-09-042-353-172
70 4 US-08-758-417A-20
45 4 US-09-425-638A-13
45 4 US-09-543-004-13

ALIGNMENTS

RESULT 1

US-09-020-846-51/c
; Sequence 51, Application US/09020846
; Patent No. 6322965
; GENERAL INFORMATION:
; APPLICANT: YAMAGUCHI, Kenjiro
; APPLICANT: KASHIWAKUMA, Tomiko
; APPLICANT: CHIBA, Yukie
; APPLICANT: YAGI, Shintaro
; APPLICANT: HASEGAWA, Akira
; TITLE OF INVENTION: CHIMERA ANTIGEN PEPTIDE
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,846
; FILING DATE: 09-FEB-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 9-027015
; FILING DATE: 10-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-024045
; FILING DATE: 09-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wegner, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 053466/0225
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
US-09-020-846-51

us-09-919-197-3.75mer.rni

Fri Nov 1 18:25:07 2002

APPLICANT: JAYASENA, SUMEDHA
 APPLICANT: GOLD, LARRY
 TITLE OF INVENTION: ENZYME LINKED OLIGONUCLEOTIDE
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson & Bratschun, L.L.C. 200
 STREET: 8400 E. Prentice Avenue, Suite 200
 CITY: Englewood
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
 COMPUTER: IBM pc compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,425
 FILING DATE:
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/714,131
 FILING DATE: 10-JUNE-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/536,428
 FILING DATE: 11-JUNE-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/964,624
 FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/234,997
 FILING DATE: 28-APRIL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 71 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All C's are 2'-NH2 cytosine

FEATURE:
 OTHER INFORMATION: All U's are 2'-NH2 uracil
 US-08-487-425-2

Query Match 1.6%; Score 23.6; DB 1; Length 71;
 Best Local Similarity 69.6%; Pred. No. 1.4e+03;
 Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 952 GCCGCTGACCCGTCTCTCTCAGCGCTCCACCTCAACTCCAT 997
 Db 63 GTCGTCTGCGCAGTCCCTCCACGTGCGCTCCACCTCAACTCCAT 18

RESULT 4
 US-08-488-402A-5/c
 Sequence 5, Application US/08488402A
 Patent No. 5837456
 GENERAL INFORMATION:
 APPLICANT: GOLD ET AL.
 TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE LIGANDS TO
 TITLE OF INVENTION: CHORIONIC GONADOTROPIN HORMONE AND RELATED GLYCOPROTEIN
 TITLE OF INVENTION: HORMONES
 NUMBER OF SEQUENCES: 160
 CORRESPONDENCE ADDRESS:

Query Match 1.7%; Score 25.4; DB 4; Length 72;
 Best Local Similarity 68.6%; Pred. No. 4.4e+02;
 Matches 35; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1081 TGTCTAGTACCTGTTCCAGCCAGCAGATCAGGTGGGAGGCTG 1131
 Db 70 TGTCTAGTACCTGTTCCAGCTACGTTAAATACCTGGCGGAGGCTG 20

RESULT 2
 US-08-983-607-45/c
 Sequence 45, Application US/08983607
 Patent No. 6140470
 GENERAL INFORMATION:
 APPLICANT: Alan Garen
 APPLICANT: Xiaohong Cai
 TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
 TITLE OF INVENTION: bodies
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Department of Molecular Biophysics
 ADDRESSEE: and Biochemistry, Yale University
 STREET: 266 Whitney Avenue
 CITY: New Haven
 STATE: Connecticut
 COUNTRY: United States of America
 ZIP: 06520-8114

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" 1.44 MB diskette
 COMPUTER: IBM PC
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Word Processing
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/983,607
 FILING DATE: April 27, 1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/IB96/01032
 FILING DATE: June 28, 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mary M. Krinsky
 REGISTRATION NUMBER: 32423
 REFERENCE/DOCKET NUMBER: OCR-679
 TELEPHONE: 203-773-9544
 TELEFAX: 203-773-1183
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 60 residues
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 DESCRIPTION: primer used in constructs

US-08-983-607-45

Query Match 1.6%; Score 23.6; DB 3; Length 60;
 Best Local Similarity 66.7%; Pred. No. 1.3e+03;
 Matches 32; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

Qy 694 TTACTCTCTAAAGAGGAGGTAGTGGGAGCTCAAGGCGGAGC 741
 Db 50 TCACCTCTCTCAGAGGCGGGTAGCGGGCGGCTGGGCGGCGGAGC 3

RESULT 3
 US-08-487-425-2/c
 Sequence 2, Application US/08487425
 Patent No. 5789163
 GENERAL INFORMATION:
 APPLICANT: DROLET, DAN

RESULT 5
 US-08-484-552A-5/c
 ; Sequence 5, Application US/08484552A
 ; Patent No. 5849890
 ; GENERAL INFORMATION:
 ; APPLICANT: GOLD, LARRY
 ; APPLICANT: JAYASENA, SUMEDHA
 ; APPLICANT: NIEUWLANDT, DAN
 ; APPLICANT: DAVIS, KEN
 ; TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE LIGANDS TO CHORIONIC
 ; TITLE OF INVENTION: GONADOTROPIN HORMONE AND RELATED GLYCOPROTEIN HORMONES
 ; NUMBER OF SEQUENCES: 160
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.
 ; STREET: 8400 E. Prentice Avenue, Suite 200

```

RESULT 6.
US-08-628-356A-4/c
; ; Sequence 4, Application US/08628356A
; ; Patent No. 5874218
; ;
; ; GENERAL INFORMATION:
; ; APPLICANT: Drolet, Daniel W.
; ; APPLICANT: Jayasena, Sumedha
; ; APPLICANT: Gold, Larry
; ; TITLE OF INVENTION: Method for Detecting a Target
; ; TITLE OF INVENTION: Compound in a Substance Using a
; ; TITLE OF INVENTION: Nucleic Acid Ligand
; ; NUMBER OF SEQUENCES: 4
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: Swanson & Bratschun, L.L.C.
; ; STREET: 8400 E. Prentice Place, Suite 200
; ; CITY: Englewood
; ; STATE: Colorado

```

Fri Nov 1 18:25:07 2002

ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disc
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,356A
FILING DATE: 05-APRIL-1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: 24-MARCH-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX54
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
OTHER INFORMATION: All C's are 2'-amino
OTHER INFORMATION: cytosine.
FEATURE:
OTHER INFORMATION: All U's are 2'-amino
OTHER INFORMATION: uridine.

US-08-628-356A-4
Query Match 1.6%; Score 23.6; DB 2; Length 71;
Best Local Similarity 69.6%; Pred. No. 1.4e+03;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 952 GCGCGCTGACCGCTGCTCTCCACGGCTCCACCTCAAGTCCAT 997
DB 63 GTCGCTGCCAGTCCCTCCACGGCTCCACACTCAGGCCCTT 18

RESULT 7
PCT-US96-07439-2/c
Sequence 2, Application PC/TUS9607439
GENERAL INFORMATION:
APPLICANT: DROLET, DAN
APPLICANT: JAYASENA, SUMEDHA
TITLE OF INVENTION: ENZYME LINKED OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07439

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,425
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/234,997
FILING DATE: 28-APRIL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX37/PCT
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
OTHER INFORMATION: All U's are 2'-NH2 uracil

PCT-US96-07439-2
Query Match 1.6%; Score 23.6; DB 5; Length 71;
Best Local Similarity 69.6%; Pred. No. 1.4e+03;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 952 GCGCGCTGACCGCTGCTCTCCACGGCTCCACCTCAAGTCCAT 997
DB 63 GTCGCTGCCAGTCCCTCCACGGCTCCACACTCAGGCCCTT 18

RESULT 8
PCT-US96-09472-5/c
Sequence 5, Application PC/TUS9609472
GENERAL INFORMATION:
APPLICANT: GOLD ET AL.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO CHORIONIC GONADOTROPIN HORMONE AND RELATED
TITLE OF INVENTION: GLYCOPROTEIN HORMONES
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09472
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,402

;; FILING DATE: 07 JUNE 1995
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/484,552
;; FILING DATE: 07 JUNE 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barry J. Swanson
;; REGISTRATION NUMBER: 33,215
;; REFERENCE/DOCKET NUMBER: NEX36-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (303) 793-3333
;; TELEFAX: (303) 793-3433
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 71 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; OTHER INFORMATION: All C's are 2'-NH2 modified
;; FEATURE:
;; OTHER INFORMATION: All U's are 2'-NH2 modified
US96-09472-5

Query Match 1.5%; Score 23.6; DB 5; Length 71;
Best Local Similarity 69.6%; Pred. No. 1.4e+03;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 952 GCGCGCTGACCGCTGCTCTCCAGCGCTCCACCTCAAGTCCAT 997
DB 63 GTCGTGCGCCAGTCCCTCCACGTGCTCCACACTCAGGCCCTT 18

RESULT 9

US-09-257-581-1/c
; Sequence 1, Application US/09257581
; Patent No. 6207419

;; GENERAL INFORMATION:
;; APPLICANT: Bauman, Frank C.
;; APPLICANT: Bauman, Susanah J.
;; TITLE OF INVENTION: THROMBIN INHIBITORY AGENTS AND METHODS OF USING SAME
;; FILE REFERENCE: 5470-232
;; CURRENT APPLICATION NUMBER: US/09/257,581
;; CURRENT FILING DATE: 1999-02-25
;; EARLIER APPLICATION NUMBER: 60/076,210
;; EARLIER FILING DATE: 1998-02-27
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1
;; LENGTH: 54
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-257-581-1

Query Match 1.5%; Score 22.4; DB 4; Length 54;
Best Local Similarity 72.5%; Pred. No. 2.6e+03;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 690 TAAATTACTCTCTAAAGGAGGAGGTAGTAGTGGAGCT 729
DB 52 TAGACCTCACCTCTAGTGGTGGTGGTGGGACT 13

RESULT 10

US-09-425-638A-38
; Sequence 38, Application US/09425638A
; Patent No. 6342587

;; GENERAL INFORMATION:
;; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
;; APPLICANT: Lloyd J. Old
;; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
;; FILE REFERENCE: LUD 5630

;; CURRENT APPLICATION NUMBER: US/09/425.638A
;; CURRENT FILING DATE: 1999-10-22
;; NUMBER OF SEQ ID NOS: 129
;; SEQ ID NO 38
;; LENGTH: 48
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
US-09-425-638A-38

Query Match 1.5%; Score 22.2; DB 4; Length 48;
Best Local Similarity 69.8%; Pred. No. 2.8e+03;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 309 GCTGTGACCTTTGAGCTGAGGCCCGCGGTGCCAGCATAC 351
DB 5 GATGGGCCCTTGGTGCAGCGCTGAGGAGCGGTGACCGGTGC 47

RESULT 11

US-09-543-004-38
; Sequence 38, Application US/09543004
; Patent No. 6346249

;; GENERAL INFORMATION:
;; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
;; APPLICANT: Lloyd J. Old
;; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THE
;; FILE REFERENCE: LUD 5630.1
;; CURRENT APPLICATION NUMBER: US/09/543,004
;; CURRENT FILING DATE: 2000-04-04
;; PRIOR APPLICATION NUMBER: 09/425,638
;; PRIOR FILING DATE: 1999-10-22
;; NUMBER OF SEQ ID NOS: 129
;; SEQ ID NO 38
;; LENGTH: 48
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
US-09-543-004-38

Query Match 1.5%; Score 22.2; DB 4; Length 48;
Best Local Similarity 69.8%; Pred. No. 2.8e+03;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 309 GCTGTGACCTTTGAGCTGAGGCCCGCGGTGCCAGCATAC 351
DB 5 GATGGGCCCTTGGTGCAGCGCTGAGGAGCGGTGACCGGTGC 47

RESULT 12

US-07-609-716-22/c
; Sequence 22, Application US/07609716
; Patent No. 5514581

;; GENERAL INFORMATION:
;; APPLICANT: Ferrari, Franco A.
;; APPLICANT: Cappello, Joseph
;; TITLE OF INVENTION: Functional Recombinant Prepared
;; TITLE OF INVENTION: Synthetic Protein Polymer
;; NUMBER OF SEQUENCES: 118
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;; STREET: Four Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: US
;; ZIP: 94111

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/609,716

FILING DATE: 06-NOV-1990
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I.
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A-55186-3/BIR
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-07-609-716-22

Query Match 1.5%; Score 22.2; DB 1; Length 61;
 Best Local Similarity 64.7%; Pred. No. 3.2e+03;
 Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 229 GGCAGCTGCTCCCGCAGCAGCGCGGCTGCTGCGAGGTTGCTGGGGCC 279
 DB 51 GCCAGAGCGCGCGCAGCTCCAGAACCGGCTCTCTGCACCGCTGCCGCGCACC 1

RESULT 13
 US-08-175-155-20/c
 Sequence 20, Application US/08175155
 Patent No. 5641648

GENERAL INFORMATION:
 APPLICANT: Ferrari, Franco A.
 APPLICANT: Cappello, Joseph
 APPLICANT: Crissman, John W.
 APPLICANT: Dorman, Mary A.
 TITLE OF INVENTION: Methods for Preparing Synthetic
 TITLE OF INVENTION: Repetitive DNA
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/175,155
 FILING DATE: 29-DEC-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I.
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A-55186-5/BIR
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-175-155-20

Query Match 1.5%; Score 22.2; DB 1; Length 61;
 Best Local Similarity 64.7%; Pred. No. 3.2e+03;

Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 229 GGCAGCTGCTCCCGCAGCAGCGCGGCTGCTGCGAGGTTGCTGGGGCC 279
 DB 51 GCCAGAGCGCGCGCAGCTCCAGAACCGGCTCTCTGCACCGCTGCCGCGCACC 1

RESULT 14

US-08-477-509B-55/c
 Sequence 55, Application US/08477509B
 Patent No. 5770697

GENERAL INFORMATION:
 APPLICANT: Ferrari, Franco A.
 APPLICANT: Cappello, Joseph
 APPLICANT: Crissman, John W.
 APPLICANT: Dorman, Mary A.
 TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
 TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
 NUMBER OF SEQUENCES: 112
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,509B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/175,155
 FILING DATE: 29-DEC-1993
 APPLICATION NUMBER: US 08/053,049
 FILING DATE: 22-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/114,618
 FILING DATE: 29-OCT-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/927,258
 FILING DATE: 04-NOV-1986
 ATTORNEY/AGENT INFORMATION:
 NAME: Trecartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 55:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-477-509B-55

Query Match 1.5%; Score 22.2; DB 1; Length 61;
 Best Local Similarity 64.7%; Pred. No. 3.2e+03;
 Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 229 GGCAGCTGCTCCCGCAGCAGCGCGGCTGCTGCGAGGTTGCTGGGGCC 279
 DB 51 GCCAGAGCGCGCGCAGCTCCAGAACCGGCTCTCTGCACCGCTGCCGCGCACC 1

RESULT 15

| | | | | | | | |
|-----------------------|--------|--------------|--------------|------------|-----|--------|-----|
| Query Match | 1.5% | Score | 22.2; | DB | 2; | Length | 61; |
| Best Local Similarity | 64.7%; | Pred. | No. 3.2e+03; | | | | |
| Matches | 33; | Conservative | 0; | Mismatches | 18; | Indels | 0; |
| Gaps | 0; | | | | | | |

Search completed: October 31, 2002, 23:18:35
Job time : 61 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 21:51:41 ; Search time 57 Seconds
(without alignments)
8510.060 Million cell updates/sec

Title: US-09-919-197-3
Perfect score: 1456
Sequence: 1 tgagcaccagccaccagg.....tatgaacactataaaaaa 1456

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 310279 seqs, 166577418 residues
1 number of hits satisfying chosen parameters: 169348

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:
1: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 26 | 1.8 | 73 | 10 | US-09-466-320-16 |
| 2 | 21 | 1.4 | 56 | 10 | US-09-944-036-30 |
| 3 | 21 | 1.4 | 64 | 10 | US-09-919-580-637 |
| 4 | 21 | 1.4 | 74 | 10 | US-09-250-611-7 |
| 5 | 20.6 | 1.4 | 70 | 10 | US-09-878-574-8527 |
| 6 | 20.4 | 1.4 | 55 | 10 | US-09-790-417-19 |
| 7 | 20.4 | 1.4 | 67 | 10 | US-09-878-574-5162 |
| 8 | 20.4 | 1.4 | 71 | 10 | US-09-783-590-2509 |
| 9 | 20.4 | 1.4 | 73 | 10 | US-09-783-590-3398 |
| 10 | 20.2 | 1.4 | 69 | 10 | US-09-983-965-3899 |
| 11 | 20 | 1.4 | 51 | 10 | US-09-874-547-8 |
| 12 | 20 | 1.4 | 70 | 10 | US-09-783-590-4790 |
| 13 | 20 | 1.4 | 75 | 10 | US-09-864-761-28813 |
| 14 | 19.8 | 1.4 | 60 | 10 | US-09-925-301-758 |
| 15 | 19.8 | 1.4 | 60 | 10 | US-09-975-408-68 |
| 16 | 19.8 | 1.4 | 60 | 12 | US-10-075-579-68 |
| 17 | 19.8 | 1.4 | 70 | 10 | US-09-822-250-30 |
| 18 | 19.8 | 1.4 | 72 | 10 | US-09-884-441-304 |
| 19 | 19.8 | 1.4 | 73 | 12 | US-10-108-280-18 |

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20 19.8 1.4 75 10 US-09-922-261-151
c 21 19.6 1.3 48 10 US-09-810-502-29
22 19.6 1.3 55 10 US-09-874-547-48
23 19.6 1.3 56 9 US-09-144-886-39
24 19.6 1.3 56 10 US-09-874-547-44
25 19.6 1.3 56 10 US-09-988-899-49
c 26 19.6 1.3 60 10 US-09-815-242-1130
c 27 19.6 1.3 71 10 US-09-783-590-5311
28 19.6 1.3 73 10 US-09-896-096A-4
29 19.6 1.3 73 10 US-09-894-924-4
c 30 19.4 1.3 55 10 US-09-920-300A-1151
c 31 19.4 1.3 55 12 US-10-033-528-1151
c 32 19.4 1.3 67 10 US-09-943-286-6
c 33 19.2 1.3 26 10 US-09-780-172-13
c 34 19.2 1.3 45 10 US-09-989-722-122
c 35 19.2 1.3 45 10 US-09-989-723-122
c 36 19.2 1.3 45 10 US-09-989-727-122
c 37 19.2 1.3 45 10 US-09-989-731-122
c 38 19.2 1.3 45 10 US-09-989-732-122
c 39 19.2 1.3 45 10 US-09-989-732-122
c 40 19.2 1.3 45 10 US-09-991-073-122
c 41 19.2 1.3 45 10 US-09-990-442-122
c 42 19.2 1.3 45 10 US-09-991-163-122
c 43 19.2 1.3 45 10 US-09-993-604-122
c 44 19.2 1.3 45 10 US-09-990-456-122
c 45 19.2 1.3 45 10 US-09-989-721-122

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ALIGNMENTS

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RESULT 1
US-09-466-320-16
; Sequence 16, Application US/09466320
; Patent No. US20020025939A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick
; TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
; FILE REFERENCE: 0450-0026.30
; CURRENT APPLICATION NUMBER: US/09/466,320
; CURRENT FILING DATE: 1999-12-17
; EARLIER APPLICATION NUMBER: US 60/112,910
; EARLIER FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: coding sequence
US-09-466-320-16

```

```

Query Match 1.8%; Score 26; DB 10; Length 73;
Best Local Similarity 62.1%; Pred. No. 3.4e+02;
Matches 41; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 186 CTGGCCACAGAGTGGCCTTCTCAGAACCTGCCATCCTCTGGAGCTGCTCCCCAG 245
Db 8 CCGTGTACAACTGGAGACCGCTGAACAATACCAACCCCTGTACACGGGCTCCCCAG 67
QY 246 GACCAG 251
Db 68 GATAAG 73

```

```

RESULT 2
US-09-944-036-30
; Sequence 30, Application US/09944036
; Patent No. US2002005095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.

```



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; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Cytomegalovirus
; FEATURE:
; OTHER INFORMATION: target for mutant cytomegalovirus
US-09-790-417-19

Query Match          1.4%; Score 20.4; DB 10; Length 55;
Best Local Similarity 61.1%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 8 CAGCCAACAGGGCGCTGCCATGCCAGGAGCTGCAAGCGCCCGCCATTCT 61
      ||||| | | | | | | | | | | | | | | | | | | | | | | |
1 CAGCAGTGGCTGAGCTTCCGGTCTCTCCGGCGGCGCAGCGCGCGGTGCT 54

RESULT 7
US-09-878-574-5162
; Sequence 5162, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Joseph R.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 5162
; LENGTH: 67
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-022-Q1-B1-D9
US-09-878-574-5162

Query Match          1.4%; Score 20.4; DB 10; Length 67;
Best Local Similarity 61.1%; Pred. No. 1.3e+04;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1403 ACTGAATTAAGTTATTGATTTTGTAAATAAAGGTATGAACACTTAAACAAA 1456
      || | ||||| | | ||||| | | | | | | | | | | | | | | | |
DB 11 ACCCAATTAAGTAACTTTTGTGCAAAAAAATAAATAAATAAATAAACA 64

RESULT 8
US-09-783-590-3398
; Sequence 3398, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3398
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (32)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-3398

Query Match          1.4%; Score 20.4; DB 10; Length 73;
Best Local Similarity 54.9%; Pred. No. 1.3e+04;
Matches 39; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

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; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2509
; LENGTH: 71
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (46)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (54)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (63)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (64)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (67)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (68)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-2509

Query Match          1.4%; Score 20.4; DB 10; Length 71;
Best Local Similarity 56.6%; Pred. No. 1.3e+04;
Matches 30; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1404 CTGAATTAAGTTATTGATTTTGTAAATAAAGGTATGAACACTTAAACAAA 1456
      | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 69 CNAANNAAAAAAATTTTNTTNAAAAAAATAAATAAATAAATAAANA 17

RESULT 9
US-09-783-590-3398
; Sequence 3398, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3398
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (32)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-3398

Query Match          1.4%; Score 20.4; DB 10; Length 73;
Best Local Similarity 54.9%; Pred. No. 1.3e+04;
Matches 39; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```

Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 415 CCCAGCCCTCCTGGCTGGCTGCAGTGGCTTCAAT 450
      |||||
db 14 CCCAGCCGGCCATGGCGAGGTCCAGTGCACAAT 49

```

RESULT 12
US-09-783-590-4790/c
Sequence 4790, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ. ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO. 4790
LENGTH: 70

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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (46)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (59)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (61)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (62)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (68)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (70)
OTHER INFORMATION: n equals a,t,g, or c
CS-09: 783-590-4790

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| Query Match | 1.4% | Score 20; | DB 10; | Length 70; |
|-----------------------|--------|--|--------|-----------------------|
| Best Local Similarity | 60.4%; | Pred. No. 1.7e+04; | | |
| Matches | 29; | Conservative | 0; | Mismatches 19; Indels |
| QY | 1409 | TTAAGTTATTGATTTTTGTAAATAAAAGGTATGAACACATAAAAAAA | 1456 | |
| b | 64 | TTNNNGCCCTTTTTTTTTTNNAAAAAATAAAAAAATAAAAAAATAAAAAA | 17 | |

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RESULT 13
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; Sequence 28813, Application US/09864761
; US-9864-761-28813/c
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIV
; TITLE OF INVENTION: GENE EXPRESSION A
; FILE REFERENCE: Acomica-x-1
;

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```

; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28813
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011815.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.57
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.49
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.51
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
; OTHER INFORMATION: EST HUMAN HIT: W45265.1, EVALUE 8.00e-35
; OTHER INFORMATION: NT HIT: X94232.1, EVALUE 6.00e-35
US-09-864-761-28813

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```

Query Match 1.4%; Score 20; DB 10; Length 75;
Best Local Similarity 65.9%; Pred. No. 1.7e+04;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 249 CAGCGGGGCTGCTGCGAGGTTGCTGGGGCCCTCTCTCTGCT 292
DB 60 CTGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17

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RESULT 14
US-09-925-301-758/c
; Sequence 758, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301

```

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; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 758
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (38)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (40)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (45)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (46)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-758

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```

Query Match 1.4%; Score 19.8; DB 10; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1421 TTTTGTGTAATAAAGGTATGAACACATAAAAAAAA 1456
DB 59 TTTTGTGTAATAAAGGTATGAACACATAAAAAAAA 24

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```

RESULT 15
US-09-975-408-68/c
; Sequence 68, Application US/09975408
; Patent No. US20020150917A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Xu, Xiao
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Kohl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
; FILE REFERENCE: 267/174 Patrick S. Eagleman
; CURRENT APPLICATION NUMBER: US/09/975,408
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/710,200
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-975-408-68

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```

Query Match 1.4%; Score 19.8; DB 10; Length 60;
Best Local Similarity 63.8%; Pred. No. 1.7e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1410 TAAGTTATTGATTTTCTGTAATAAAGGTATGAACACATAAAAAAAA 1456
DB 48 TCAGTATTGATTTGTAATAAAGGTATGAACACATAAAAAAAA 2

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Search completed: October 31, 2002, 23:19:53
Job time : 59 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 21:09:57 ; Search time 1937 Seconds
(without alignments)
12173.789 Million cell updates/sec

Title: US-09-919-197-3

Perfect score: 1456

Sequence: 1 ttagcaccagccaccagg.....tatgaacactaaaaaaa 1456

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

al number of hits satisfying chosen parameters: 218680

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpi: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| C 1 | 32.4 | 2.2 | 34 | 9 | A1221747 |
| C 2 | 29.8 | 2.0 | 62 | 17 | B37921 |
| C 3 | 28.8 | 2.0 | 57 | 13 | BI745330 |
| C 4 | 28.2 | 1.9 | 52 | 9 | AA782923 |
| C 5 | 27.6 | 1.9 | 72 | 13 | BI260363 |
| C 6 | 26.8 | 1.8 | 68 | 12 | BF632727 |

| | | | | | | | |
|---|----|------|-----|----|----|-----------|--------------------|
| C | 7 | 26.6 | 1.8 | 53 | 14 | H55352 | H55352 CHR20291 C |
| | 8 | 26.2 | 1.8 | 35 | 14 | R37139 | R37139 vF54g11.s1 |
| | 9 | 26.2 | 1.8 | 55 | 9 | AI123105 | AI123105 qa85b11.s |
| | 10 | 26.2 | 1.8 | 60 | 14 | R85541 | R85541 y038c03.s1 |
| | 11 | 25.8 | 1.8 | 47 | 14 | H97244 | H97244 yv98e05.s1 |
| | 12 | 25.6 | 1.8 | 46 | 9 | AA916309 | AA916309 on64a06.s |
| | 13 | 25.4 | 1.7 | 61 | 12 | BF581452 | BF581452 602100856 |
| C | 14 | 25.4 | 1.7 | 63 | 10 | AW333106 | AW333106 S17D5 AGS |
| | 15 | 25.2 | 1.7 | 47 | 14 | N67514 | N67514 za08g10.s1 |
| | 16 | 25.2 | 1.7 | 69 | 17 | CNS0214K | AL198461 Tetraodon |
| | 17 | 25 | 1.7 | 65 | 17 | AZ664880 | AZ664880 TM0545H01 |
| | 18 | 25 | 1.7 | 74 | 9 | AA574536 | AA574536 vm29e03.r |
| C | 19 | 24.8 | 1.7 | 46 | 9 | AA853962 | AA853962 aj51e02.s |
| C | 20 | 24.8 | 1.7 | 61 | 9 | AI144267 | AI144267 qb59e02.x |
| C | 21 | 24.8 | 1.7 | 67 | 10 | AW633089 | AW633089 bl03f09.x |
| C | 22 | 24.8 | 1.7 | 67 | 17 | AZ397521 | AZ397521 LM0162J05 |
| C | 23 | 24.8 | 1.7 | 75 | 14 | N68192 | N68192 zal1f07.s1 |
| C | 24 | 24.6 | 1.7 | 67 | 9 | AI366713 | AI366713 qy95b04.x |
| C | 25 | 24.6 | 1.7 | 73 | 9 | AA987684 | AA987684 q088a08.s |
| C | 26 | 24.4 | 1.7 | 70 | 14 | BQ454399 | BQ454399 ke04b11.y |
| C | 27 | 24.2 | 1.7 | 63 | 9 | AI274192 | AI274192 ql46b08.x |
| C | 28 | 24.2 | 1.7 | 71 | 14 | T25646 | T25646 EST00515 Eq |
| C | 29 | 24 | 1.6 | 64 | 9 | AI448858 | AI448858 ms45f07.x |
| C | 30 | 24 | 1.6 | 69 | 17 | CNS0214K | AL198461 Tetraodon |
| C | 31 | 24 | 1.6 | 72 | 9 | AA809609 | AA809609 nz17e02.s |
| C | 32 | 23.8 | 1.6 | 59 | 10 | AW168138 | AW168138 xg60d06.x |
| C | 33 | 23.8 | 1.6 | 65 | 9 | AI903143 | AI903143 QV-BT022- |
| C | 34 | 23.8 | 1.6 | 66 | 9 | AI887645 | AI887645 wml6d11.x |
| C | 35 | 23.8 | 1.6 | 67 | 2 | HSM011809 | AI046959 Homo sapi |
| C | 36 | 23.8 | 1.6 | 69 | 9 | AL675639 | AL675639 AL675639 |
| C | 37 | 23.8 | 1.6 | 70 | 9 | AA785915 | AA785915 l2h03a1.f |
| C | 38 | 23.8 | 1.6 | 73 | 9 | AI468883 | AI468883 ti43e02.x |
| C | 39 | 23.8 | 1.6 | 75 | 14 | R52050 | R52050 vj71d12.r1 |
| C | 40 | 23.6 | 1.6 | 65 | 9 | AA599569 | AA599569 ag08c08.s |
| C | 41 | 23.6 | 1.6 | 67 | 14 | H47793 | H47793 yp80e06.r1 |
| C | 42 | 23.6 | 1.6 | 70 | 9 | AI250258 | AI250258 qx03a04.x |
| C | 43 | 23.6 | 1.6 | 72 | 10 | AV948273 | AV948273 AV948273 |
| C | 44 | 23.6 | 1.6 | 72 | 14 | BQ394194 | BQ394194 NISC-ng07 |
| C | 45 | 23.4 | 1.6 | 53 | 9 | AA632173 | AA632173 np63a07.s |

ALIGNMENTS

RESULT 1
A1221747/c A1221747 34 bp mRNA linear EST 30-NOV-1998
LOCUS qg93f02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1842747 3', similar to TR:Q15466 Q15466 NUCLEAR HORMONE
RECEPTOR ;, mRNA sequence.
ACCESSION A1221747
VERSION A1221747.1 GI:3803950
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 34)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-re@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 990 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..34
/organism="Homo sapiens"

QY 565 TGCCCAAGTCACCCAGCTAAATAGTGACAGTCTGGGATTTCATACCAGGAGCCT 621
|||||
Db 60 TGCCCAAGTCACCCAGCTAAATAGTGACAGTCTGGGATTTCATACCAGGAGCCT 4
|||||

RESULT 3
B1745330 57 bp mRNA linear EST 25-SEP-2001
LOCUS
DEFINITION
rK99b01.y1 Meloidogynae javanica egg pAMP1 v6 Chiapelli McCarter
Meloidogynae javanica cDNA 5', mRNA sequence.
ACCESSION
B1745330
VERSION
B1745330.1 GI:15767132
KEYWORDS
EST.
SOURCE
root-knot nematode.
ORGANISM
Meloidogynae javanica
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchida;
Tylenchoidea; Heterodera; Meloidogyninae; Meloidogynae.
REFERENCE
1 (bases 1 to 57)
AUTHORS
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.,
Dante, M., Marr, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,
Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagaris, V., R.,
Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe,
M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,
Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
JOURNAL
COMMENT
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapell@watson.wustl.edu & jmcarter@watson.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.

FEATURES
source
1..57
/organism="Meloidogynae javanica"
/db_xref="taxon:6303"
/clone_lib="Meloidogynae javanica egg pAMP1 v6 Chiapelli
McCarter"
/dev_stage="enriched for eggs"
/lab_host="DH10B"
/note="vector: pAMP1 (Gibco); The library was constructed
by Brandi Chiapelli and Dr. James McCarter at Washington
University, St. Louis. The cDNA was made by using Dynabead
oligo-dt priming (Dyna), PCR based library using a
modified protocol from the SMART PCR cDNA Synthesis kit
from Clontech. Directionally cloned into the UDG sites of
pAMP1. Nematodes were provided by Dr. David Bird of North
Carolina State University."
BASE COUNT 26 a 1 c 4 g 26 t
ORIGIN

Query Match 2.0%; Score 28.8; DB 13; Length 57;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 36; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1409 TTAAGCTTTATTTTCTTAATAAAAGGTATGAAACACTAAAAAAA 1456
|||||
Db 7 TTCAATTATTATTTTCTTAATAAAAGGTATGAAACACTAAAAAAA 54
|||||

RESULT 4
AA782923 52 bp mRNA linear EST 05-FEB-1998
LOCUS
DEFINITION
ai62c05.s1 Soares testis NHT Homo sapiens cDNA clone 1375400 3/
similar to gb:X57025.rnal INSULIN-LIKE GROWTH FACTOR IA PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION
AA782923

/db_xref="taxon:9606"
/clone="IMAGE:1842747"
/clone_lib="Soares_NFL_T_GRC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site:1: Not I; Site:2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19w, testis NHT, and B-cell
NCI-CGAP-GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
6 a 6 c 16 g 6 t

BASE COUNT
ORIGIN

Query Match 2.2%; Score 32.4; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 1.6e+03;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 978 GCCTCCAGCCCTCAAGTCATCCGACGAGCTGC 1011
|||||
Db 34 GCCTCCAGCCCTCAAGTCATCCGACGAGCTGC 1
|||||

RESULT 2
B37921/c 62 bp DNA linear GSS 18-OCT-1997
LOCUS
DEFINITION
HS-1046-A2-G04-MR.abi CIT Human Genomic Sperm Library C Homo
sapiens genomic clone Plate-CT 829 Col-8 Row-M; DNA sequence.
ACCESSION
B37921
VERSION
B37921.1 GI:2542173
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 62)
AUTHORS
Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S.,
Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
Unpublished (1997)
JOURNAL
COMMENT
Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackrone@u.washington.edu
Sequence Tagged Connector
Plate: CT 829 row: M column: 8
Class: BAC ends
High quality sequence stop: 62.
Location/Qualifiers
1..62
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Human Genomic Sperm Library C"
/clone="Plate-CT 829 Col-8 Row=M"
/sex="M"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

BASE COUNT
ORIGIN

Query Match 2.0%; Score 29.8; DB 17; Length 62;
Best Local Similarity 70.2%; Pred. No. 7.5e+03;
Matches 40; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11263 row: h column: 03
High quality sequence stop: 72.
Location/Qualifiers
1. 72
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5108786"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: PCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 Kb. Library prepared by Life
Technologies."
BASE COUNT 44 a 4 c 6 g 18 t
ORIGIN
Query Match. 1.9%; Score 27.6; DB 13; Length 72;
Best Local Similarity 63.6%; Pred. No. 2.7e+04;
Matches 42; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1391 ACCTTATACAGACTCAATTAAGTTATTGATTTTGTAAATAAAGGTATGAACACTAAA 1450
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ACAGTTTACAGAAATAAATGTTTTTTTTCAGAAAAAATAAAAAACAAAAA 60
QY 1451 AAAAAA 1456
|||||
Db 61 AAAAAA 66

RESULT 6
BF632727/c
LOCUS
DEFINITION
5', mRNA sequence..
BF632727 68 bp mRNA linear EST 19-DEC-2000
BF632727.1 GI:11896885
EST.
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1. (bases 1 to 68)
Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula drought library
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 68 Std Error: 0.00
Plate: 046 row: A column: 08
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
1..68
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF046A08DT"
/tissue_type="Drought"
/clone_lib="Drought"
/tissue_type="plantlets"
FEATURES
Source

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